

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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- (ii) TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
- (iii) NUMBER OF SEQUENCES: 148
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/023,082
 - (B) FILING DATE: 13-FEB-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US95/01790
 - (B) FILING DATE: 14-FEB-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/461,195
 - (B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/023,852
 - (B) FILING DATE: 13-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/039,045
 - (B) FILING DATE: 28-FEB-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/862,432
- (B) FILING DATE: 23-MAY-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/910,875
- (B) FILING DATE: 13-AUG-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/055,561
- (B) FILING DATE: 13-AUG-1997

(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-371-2600
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
CCC GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC	96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
GTC CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
GCC ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	
50 55 60	

AGG CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
AAG CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
AAG GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA	432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	
130 135 140	
GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA	480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	
145 150 155 160	
TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG	528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	
165 170 175	
TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA	576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	
180 185 190	
CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
TAG	627

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15
Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu
		35					40					45			
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly
	50					55					60				
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
65					70					75					80
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
				85					90					95	
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
			100					105					110		
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
	115						120					125			
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
	130					135					140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150					155					160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
				165					170					175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180					185					190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCACATGT GGAAATGGAT ACTGACACAT TGTGCC

36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGCCATGG CGTGCCAAGC CCTTGGTCAG GACATG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGGATCCG CCATCATGTG GAAATGGATA CTCAC

35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGCGGTACC ACAAACGTTG CCTTCCT

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAACGAGGAT CCGCCATCAT GTGGAAATGG ATACTGACAC

40

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAAGCACTCG AGTGAGTGTA CCACCATTGG AAGAAATG

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTAACCCTC ACTAAAGGGA GGCCATGTGG AAATGGATAC TGACACATTG TGCC

54

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ser Gly Pro Gly Thr Ala Ala Val Ala Leu Leu Pro Ala Val Leu
1 5 10 15

Leu	Ala	Leu	Leu	Ala	Pro	Trp	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Ala	Pro	20	25	30
Thr	Ala	Pro	Asn	Gly	Thr	Leu	Glu	Ala	Glu	Leu	Glu	Arg	Arg	Trp	Glu	35	40	45
Ser	Leu	Val	Ala	Leu	Ser	Leu	Ala	Arg	Leu	Pro	Val	Ala	Ala	Gln	Pro	50	55	60
Lys	Glu	Ala	Ala	Val	Gln	Ser	Gly	Ala	Gly	Asp	Tyr	Leu	Leu	Gly	Ile	65	70	75
Lys	Arg	Leu	Arg	Arg	Leu	Tyr	Cys	Asn	Val	Gly	Ile	Gly	Phe	His	Leu	85	90	95
Gln	Ala	Leu	Pro	Asp	Gly	Arg	Ile	Gly	Gly	Ala	His	Ala	Asp	Thr	Arg	100	105	110
Asp	Ser	Leu	Leu	Glu	Leu	Ser	Pro	Val	Glu	Arg	Gly	Val	Val	Ser	Ile	115	120	125
Phe	Gly	Val	Ala	Ser	Arg	Phe	Phe	Val	Ala	Met	Ser	Ser	Lys	Gly	Lys	130	135	140
Leu	Tyr	Gly	Ser	Pro	Phe	Phe	Thr	Asp	Glu	Cys	Thr	Phe	Lys	Glu	Ile	145	150	155
Leu	Leu	Pro	Asn	Asn	Tyr	Asn	Ala	Tyr	Glu	Ser	Tyr	Lys	Tyr	Pro	Gly	165	170	175
Met	Phe	Ile	Ala	Leu	Ser	Lys	Asn	Gly	Lys	Thr	Lys	Lys	Gly	Asn	Arg	180	185	190
Val	Ser	Pro	Thr	Met	Lys	Val	Thr	His	Phe	Leu	Pro	Arg	Leu			195	200	205

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ser	Arg	Gly	Ala	Gly	Arg	Leu	Gln	Gly	Thr	Leu	Trp	Ala	Leu	Val	1	5	10	15
Phe	Leu	Gly	Ile	Leu	Val	Gly	Met	Val	Val	Pro	Ser	Pro	Ala	Gly	Thr				

20	25	30
Arg Ala Asn Asn Thr Leu Leu Asp Ser Arg Gly Trp Gly Thr Leu Leu		
35	40	45
Ser Arg Ser Arg Ala Gly Leu Ala Gly Glu Ile Ala Gly Val Asn Trp		
50	55	60
Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys		
65	70	75
Asn Val Gly Ile Gly Phe His Leu Gln Val Leu Pro Asp Gly Arg Ile		
85	90	95
Ser Gly Thr His Glu Glu Asn Pro Tyr Ser Leu Leu Glu Ile Ser Thr		
100	105	110
Val Glu Arg Gly Val Val Ser Leu Phe Gly Val Arg Ser Ala Leu Phe		
115	120	125
Val Ala Met Asn Ser Lys Gly Arg Leu Tyr Ala Thr Pro Ser Phe Gln		
130	135	140
Glu Glu Cys Lys Phe Arg Glu Thr Leu Leu Pro Asn Asn Tyr Asn Ala		
145	150	155
Tyr Glu Ser Asp Leu Tyr Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr		
165	170	175
Gly Arg Val Lys Arg Gly Ser Lys Val Ser Pro Ile Met Thr Val Thr		
180	185	190
His Phe Leu Pro Arg Ile		
195		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ser Leu Ser Phe Leu Leu Leu Leu Phe Phe Ser His Leu Ile Leu		
1	5	10
Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro		
20	25	30

(2) INFORMATION FOR SEQ ID NO:16:

(A) LENGTH: 155 amino acids

(C) STRANDEDNESS: no

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

;

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Ala	Glu	Gly	Glu	Ile	Thr	Thr	Phe	Thr	Ala	Leu	Thr	Glu	Lys	Phe	1	5	10	15
Asn	Leu	Pro	Pro	Gly	Asn	Tyr	Lys	Lys	Pro	Lys	Leu	Leu	Tyr	Cys	Ser	20	25	30	
Asn	Gly	Gly	His	Phe	Leu	Arg	Ile	Leu	Pro	Asp	Gly	Thr	Val	Asp	Gly	35	40	45	
Thr	Arg	Asp	Arg	Ser	Asp	Gln	His	Ile	Gln	Leu	Gln	Leu	Ser	Ala	Glu	50	55	60	
Ser	Val	Gly	Glu	Val	Tyr	Ile	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Tyr	Leu	65	70	75	80
Ala	Met	Asp	Thr	Asp	Gly	Leu	Leu	Tyr	Gly	Ser	Gln	Thr	Pro	Asn	Glu	85	90	95	
Glu	Cys	Leu	Phe	Leu	Glu	Arg	Leu	Glu	Glu	Asn	His	Tyr	Asn	Thr	Tyr	100	105	110	
Ile	Ser	Lys	Lys	His	Ala	Glu	Lys	Asn	Trp	Phe	Val	Gly	Leu	Lys	Lys	115	120	125	
Asn	Gly	Ser	Cys	Lys	Arg	Gly	Pro	Arg	Thr	His	Tyr	Gly	Gln	Lys	Ala	130	135	140	
Ile	Leu	Phe	Leu	Pro	Leu	Pro	Val	Ser	Ser	Asp	145	150	155						

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ala	Ala	Gly	Ser	Ile	Thr	Thr	Leu	Pro	Ala	Leu	Pro	Glu	Asp	Gly	1	5	10	15
Gly	Ser	Gly	Ala	Phe	Pro	Pro	Gly	His	Phe	Lys	Asp	Pro	Lys	Arg	Leu	20	25	30	

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
35 40 45

Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
50 55 60

Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65 70 75 80

Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
85 90 95

Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
100 105 110

Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
115 120 125

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
130 135 140

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala
1 5 10 15

Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
20 25 30

Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
35 40 45

Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
50 55 60

Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
65 70 75 80

Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu

	85		90		95
Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser					
	100		105		110
Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu					
	115		120		125
Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp					
	130		135		140
Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg					
145		150		155	160
Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr					
	165		170		175
Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val					
	180		185		190
Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser					
	195		200		205

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg			
1	5	10	15
Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys			
	20	25	30
Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser			
	35	40	45
Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile			
	50	55	60
Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp			
	65	70	75
Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn			

	85		90		95
Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly					
	100		105		110
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr					
	115		120		125
Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu					
	130		135		140
Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly					
145		150		155	160
Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly					
	165		170		175
Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala					
	180		185		190
Ile Thr					

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu			
1	5	10	15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser			
	20	25	30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu			
	35	40	45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly			
	50	55	60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg			
65	70	75	80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly			
	85	90	95

Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
			100					105					110		
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
		115					120					125			
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
	130					135					140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150					155					160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
				165					170					175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180					185					190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Gly	Leu	Ile	Trp	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Glu	Pro	Gly	Trp
1				5					10					15	
Pro	Ala	Ala	Gly	Pro	Gly	Ala	Arg	Leu	Arg	Arg	Asp	Ala	Gly	Gly	Arg
			20					25					30		
Gly	Gly	Val	Tyr	Glu	His	Leu	Gly	Gly	Ala	Pro	Arg	Arg	Arg	Lys	Leu
		35					40						45		
Tyr	Cys	Ala	Thr	Lys	Tyr	His	Leu	Gln	Leu	His	Pro	Ser	Gly	Arg	Val
	50					55					60				
Asn	Gly	Ser	Leu	Glu	Asn	Ser	Ala	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ala
65					70					75				80	
Val	Glu	Val	Gly	Ile	Val	Ala	Ile	Arg	Gly	Leu	Phe	Ser	Gly	Arg	Tyr
				85					90					95	

Leu	Ala	Met	Asn	Lys	Arg	Gly	Arg	Leu	Tyr	Ala	Ser	Glu	His	Tyr	Ser
			100					105					110		
Ala	Glu	Cys	Glu	Phe	Val	Glu	Arg	Ile	His	Glu	Leu	Gly	Tyr	Asn	Thr
		115					120					125			
Tyr	Ala	Ser	Arg	Leu	Tyr	Arg	Thr	Val	Ser	Ser	Thr	Pro	Gly	Ala	Arg
		130				135					140				
Arg	Gln	Pro	Ser	Ala	Glu	Arg	Leu	Trp	Tyr	Val	Ser	Val	Asn	Gly	Lys
145					150					155					160
Gly	Arg	Pro	Arg	Arg	Gly	Phe	Lys	Thr	Arg	Arg	Thr	Gln	Lys	Ser	Ser
				165					170					175	
Leu	Phe	Leu	Pro	Arg	Val	Leu	Asp	His	Arg	Asp	His	Glu	Met	Val	Arg
			180					185					190		
Gln	Leu	Gln	Ser	Gly	Leu	Pro	Arg	Pro	Pro	Gly	Lys	Gly	Val	Gln	Pro
		195					200					205			
Arg	Arg	Arg	Arg	Gln	Lys	Gln	Ser	Pro	Asp	Asn	Leu	Glu	Pro	Ser	His
		210				215					220				
Val	Gln	Ala	Ser	Arg	Leu	Gly	Ser	Gln	Leu	Glu	Ala	Ser	Ala	His	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Gly	Ser	Pro	Arg	Ser	Ala	Leu	Ser	Cys	Leu	Leu	Leu	His	Leu	Leu
1				5					10					15	
Val	Leu	Cys	Leu	Gln	Ala	Gln	Val	Arg	Ser	Ala	Ala	Gln	Lys	Arg	Gly
		20						25					30		
Pro	Gly	Ala	Gly	Asn	Pro	Ala	Asp	Thr	Leu	Gly	Gln	Gly	His	Glu	Asp
		35					40					45			
Arg	Pro	Phe	Gly	Gln	Arg	Ser	Arg	Ala	Gly	Lys	Asn	Phe	Thr	Asn	Pro
		50				55					60				
Ala	Pro	Asn	Tyr	Pro	Glu	Glu	Gly	Ser	Lys	Glu	Gln	Arg	Asp	Ser	Val

65		70		75		80									
Leu	Pro	Lys	Val	Thr	Gln	Arg	His	Val	Arg	Glu	Gln	Ser	Leu	Val	Thr
				85					90					95	
Asp	Gln	Leu	Ser	Arg	Arg	Leu	Ile	Arg	Thr	Tyr	Gln	Leu	Tyr	Ser	Arg
			100					105					110		
Thr	Ser	Gly	Lys	His	Val	Gln	Val	Leu	Ala	Asn	Lys	Arg	Ile	Asn	Ala
		115					120					125			
Met	Ala	Glu	Asp	Gly	Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
		130				135					140				
Thr	Phe	Gly	Ser	Arg	Val	Arg	Val	Arg	Gly	Ala	Glu	Thr	Gly	Leu	Tyr
145					150					155					160
Ile	Cys	Met	Asn	Lys	Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys
			165					170						175	
Gly	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
			180					185					190		
Ala	Leu	Gln	Asn	Ala	Lys	Tyr	Glu	Gly	Trp	Tyr	Met	Ala	Phe	Thr	Arg
		195					200					205			
Lys	Gly	Arg	Pro	Arg	Lys	Gly	Ser	Lys	Thr	Arg	Gln	His	Gln	Arg	Glu
		210				215					220				
Val	His	Phe	Met	Lys	Arg	Leu	Pro	Arg	Gly	His	His	Thr	Thr	Glu	Gln
225					230					235					240
Ser	Leu	Arg	Phe	Glu	Phe	Leu	Asn	Tyr	Pro	Pro	Phe	Thr	Arg	Ser	Leu
			245					250						255	
Arg	Gly	Ser	Gln	Arg	Thr	Trp	Ala	Pro	Glu	Pro	Arg				
			260					265							

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 593..1216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA	60
CAACTCCAAA GGGATATACT TGTAAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA	120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC	180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG	240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA	300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA	360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG	420
CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCCAGAGG	480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT	540
CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG	595
	Met
	1
TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC	643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro	
	5 10 15
GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC	691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val	
	20 25 30
CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC	739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala	
	35 40 45
ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG	787
Thr Asn Ser Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg	
	50 55 60 65
CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG	835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys	
	70 75 80
CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG	883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys	
	85 90 95
GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA	931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile	
	100 105 110
ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC	979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn	
	115 120 125
TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA	1027

Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu	
130 135 140 145	
TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC	1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr	
150 155 160	
AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT	1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	
165 170 175	
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA	1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	
180 185 190	
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTTGTTGT TGTGTCAAG TTTTTGTTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTA CTGGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTTC TAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296

TTCTTGCCAA ATGTCATGGC GGTAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416
CCCAGGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT AAAAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTTCCC	3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTTTCATC ATACTTTGCT TCCAACCTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTTGTG GTTGGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAACCTAGGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TGCCTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976

GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA 4036
 ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAG CAGTTTCAGC 4096
 CCTGAATGTT GTAGATTTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156
 TTCGCCCTAT AGTGAGTCGT A 4177

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu	1	5	10	15
Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Val	Ser	Ser	20	25	30	
Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	35	40	45	
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	50	55	60	
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	65	70	75	80
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	85	90	95	
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	100	105	110	
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	115	120	125	
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	130	135	140	
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	145	150	155	160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	165	170	175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	180	185	190	

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
1 5 10 15

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
1 5 10 15

Pro Tyr Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys
1				5					10					15	
Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn
1				5					10					15	
Thr	Ser	Ala													

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG	AGA	GGA	TCG	CAT	CAC	CAT	CAC	CAT	CAC	GGA	TCC	TGC	CAG	GCT	CTG
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Cys	Gln	Ala	Leu
1				5					10					15	

GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC AAC TCT TCC TCT TCC TCT	96
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser	
20 25 30	
TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC	144
Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His	
35 40 45	
CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC	192
Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr	
50 55 60	
TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG	240
Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu	
65 70 75 80	
AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT	288
Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val	
85 90 95	
GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG	336
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys	
100 105 110	
AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG	384
Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	
115 120 125	
AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC	432
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
130 135 140	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA	480
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
145 150 155 160	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC	528
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
165 170 175	
TTT CTT CCA ATG GTG GTA CAC TCA TAG	555
Phe Leu Pro Met Val Val His Ser	
180	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Cys	Gln	Ala	Leu	1	5	10	15
Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	20	25	30	
Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	Arg	His	Val	Arg	Ser	Tyr	Asn	His	35	40	45	
Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	50	55	60	
Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	65	70	75	80
Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	85	90	95	
Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	100	105	110	
Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	115	120	125	
Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	130	135	140	
Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	145	150	155	160
Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	165	170	175	
Phe	Leu	Pro	Met	Val	Val	His	Ser	180											

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGTGGAAAT GGATACTGAC CCACTGCGCT TCTGCTTTCC CGCACCTGCC GGGTTGCTGC

TGCTGCTGCT TCCTGCTGCT GTTC

84

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCGGAGAAAC CATGTCCTGA CCCAGAGCCT GGCAGGTAAC CGGAACAGAA GAAACCAGGA 60

ACAGCAGCAG GAAGCAGCAG CA 82

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGTCAGGAC ATGGTTTCTC CGGAAGCTAC CAACTCTTCT TCTTCTTCTT TCTCTTCTCC 60

GTCTTCTGCT GGTCGTCACG 80

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTGAAAGAG AACAGTTTAC GCCAACGAAC GTCACCCTGC AGGTGGTTGT AAGAACGAAC 60

GTGACGACCA GCAGAAGACG G 81

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA 60

GTTTCTGGGA CAAA 75

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTGGTCCCA GAAACTTTAC CGTTTTTTTC GATTTTCAG 39

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAAGGATCCA TGTGGAAATG GATACTGACC CACTGC

36

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG TGG AAA TGG ATA CTG ACC CAC TGC GCT TCT GCT TTC CCG CAC CTG	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
CCG GGT TGC TGC TGC TGC TGC TTC CTG CTG CTG TTC CTG GTT TCT TCT	96
Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
GTT CCG GTT ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
GCT ACC AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG ACT TCC GCT GGT	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly	
50 55 60	
CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA	432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	
130 135 140	

[illegible]

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu
1				5					10					15	
Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Val	Ser	Ser
			20					25					30		
Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu
		35					40					45			
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Thr	Ser	Ala	Gly
	50					55					60				
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
65					70					75					80
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
				85					90					95	
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
			100					105					110		
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
		115					120					125			
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys

130		135		140
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly				
145		150		155
				160
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met				
	165		170	175
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr				
	180		185	190
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser				
	195		200	205

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTCATGACT TGTCAAGCTC TGGGTCAAGA TATGGTTC

38

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCCAAGCTT CCACAAACGT TGCCTTCC

28

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	522

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

TAG

525

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCAGTGAATT CATTAAAGAG GAGAAATTAA TCATGACTTG CCAGG

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCATGACTTG CCAGGCACTG GGTCAAGACA TGGTTTCCCC GGAAGCTA

48

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTTCAGCAG CCCATCTAGC GCAGGTCGTC ACGTTCGCTC TTACAACC

48

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTTCGTTGGC GCAAACGTGT CAGCTTTACC AAGTACTTCC TGAAAATC

48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGAAAAAAA CGGTAAAGTT TCTGGGAC

28

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGGCTGC TGAAGCTAGA GCTGGAGCTG TTGGTAGCTT CCGGGGAA

48

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AACAGTTTGC GCCAACGAAC ATCACCTGT AAGTGGTTGT AAGAG

45

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCTTGGTCC CAGAACTTT ACCGTTTTTT TCGATTTTCA GGAAGTA

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTCTTGGTCC CAGAACTTT ACCG

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGATCAGGCT TCTATTATTA TGAGTGTAAC ACCATTGGAA GAAAG

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG ACT TGC CAG GCA CTG GGT CAA GAC ATG GTT TCC CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC AGC TCC AGC TCT AGC TTC AGC AGC CCA TCT AGC GCA GGT CGT CAC	96
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGC TCT TAC AAC CAC TTA CAG GGT GAT GTT CGT TGG CGC AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC AGC TTT ACC AAG TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA 522
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

TAG 525

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC

35

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGACAGCCAT GGCTGGTCGT CACGTTCTG

28

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGACAGCCAT GGTTTCGTTGG CGTAAACTG

29

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGACAGCCAT GGAAAAAAAC GGTAAAGTTT C

31

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGACCCCCAT GGAGAACTGC CCGTAGAGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGACCCCCAT GGTCAAAGCC ATTAACAGCA AC

32

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGACCCCCAT GGGGAAACTC TATGGCTCAA AAG

33

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGCCCAAGC TTATTACTTC AGCTTACAGT CATTGT

36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	522
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
165 170	
TAG	525

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT	48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val	
1 5 10 15	
CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA	96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu	
20 25 30	
AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC	144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser	
35 40 45	
ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC	192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala	
50 55 60	
ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT	240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr	
65 70 75 80	
GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG	288
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu	
85 90 95	
GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG	336
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly	
100 105 110	
AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA	384
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly	
115 120 125	
CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG	432
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val	
130 135 140	
GTA CAC TCA TAG	444
Val His Ser	
145	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
 1             5             10             15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
          20             25             30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
          35             40             45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
          50             55             60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
          65             70             75             80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
          85             90             95
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
          100             105             110
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
          115             120             125
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
          130             135             140
Val His Ser
          145

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

ATG GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA      48
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
 1             5             10             15
ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG      96

```

Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	
			20					25					30			
TAC	AGC	ATC	CTG	GAG	ATA	ACA	TCA	GTA	GAA	ATC	GGA	GTT	GTT	GCC	GTC	144
Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	
		35					40				45					
AAA	GCC	ATT	AAC	AGC	AAC	TAT	TAC	TTA	GCC	ATG	AAC	AAG	AAG	GGG	AAA	192
Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	
	50					55				60						
CTC	TAT	GGC	TCA	AAA	GAA	TTT	AAC	AAT	GAC	TGT	AAG	CTG	AAG	GAG	AGG	240
Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	
	65				70				75						80	
ATA	GAG	GAA	AAT	GGA	TAC	AAT	ACC	TAT	GCA	TCA	TTT	AAC	TGG	CAG	CAT	288
Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	
			85					90					95			
AAT	GGG	AGG	CAA	ATG	TAT	GTG	GCA	TTG	AAT	GGA	AAA	GGA	GCT	CCA	AGG	336
Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	
		100					105					110				
AGA	GGA	CAG	AAA	ACA	CGA	AGG	AAA	AAC	ACC	TCT	GCT	CAC	TTT	CTT	CCA	384
Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	
	115						120					125				
ATG	GTG	GTA	CAC	TCA	TAG											402
Met	Val	Val	His	Ser												
	130															

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Val	Arg	Trp	Arg	Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	
1				5					10					15		
Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	
			20					25					30			
Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	
	35					40					45					
Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	
	50					55				60						

Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg
65					70					75					80
Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His
			85						90					95	
Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg
			100					105					110		
Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro
		115					120					125			
Met	Val	Val	His	Ser											
			130												

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG	48
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	
1 5 10 15	
TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC	96
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	
20 25 30	
AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA	144
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	
35 40 45	
CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG	192
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	
50 55 60	
ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT	240
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	
65 70 75 80	
AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG	288
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	

85	90	95	
AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA			336
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro			
100	105	110	
ATG GTG GTA CAC TCA TAG			354
Met Val Val His Ser			
115			

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	
1				5				10					15			
Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	
			20					25					30			
Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	
			35					40				45				
Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	
	50						55				60					
Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	
65					70				75					80		
Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	
				85					90					95		
Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	
			100					105					110			
Met	Val	Val	His	Ser												
			115													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEO ID NO:73:

ATG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC 48
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile
185 190 195 200

GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG 96
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met
205 210 215

AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT 144
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
220 225 230

AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA 192
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser
235 240 245

TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA 240
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly
250 255 260

AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT 288
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser
265 270 275 280

GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA TAG 321
Ala His Phe Leu Pro Met Val Val His Ser
285 290

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile
1 5 10 15

Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met
20 25 30

Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys

35	40	45
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser		
50	55	60
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly		
65	70	75
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser		
85	90	95
Ala His Phe Leu Pro Met Val Val His Ser		
100	105	

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATG GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG	48
Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys	
1 5 10 15	
GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG	96
Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys	
20 25 30	
GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG	144
Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp	
35 40 45	
CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT	192
Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala	
50 55 60	
CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT	240
Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe	
65 70 75 80	
CTT CCA ATG GTG GTA CAC TCA TAG	264

Leu Pro Met Val Val His Ser
85

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	
1				5					10					15		
Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	
			20					25					30			
Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	
		35					40					45				
Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	
	50					55					60					
Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	
	65				70					75					80	
Leu	Pro	Met	Val	Val	His	Ser										
					85											

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATG	GGG	AAA	CTC	TAT	GGC	TCA	AAA	GAA	TTT	AAC	AAT	GAC	TGT	AAG	CTG	
Met	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	
1				5					10					15		

AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC	96
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA	144
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC	192
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
TTT CTT CCA ATG GTG GTA CAC TCA TAG	219
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	
1 5 10 15	
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG	357
Asn Asn Asp Cys Lys Leu Lys	
115	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

Asn Asn Asp Cys Lys Leu Lys
115

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT	48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val	
1 5 10 15	
CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA	96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu	
20 25 30	
AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC	144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser	
35 40 45	
ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC	192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala	
50 55 60	
ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT	240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr	
65 70 75 80	

GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG
 Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
 85 90

276

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
 1 5 10 15
 Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
 20 25 30
 Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
 35 40 45
 Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
 50 55 60
 Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
 65 70 75 80
 Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGACCTCTC AGGCTCTGGG TCAGGACATG GTTTCTCCGG AAGCTACCAA CTCTTCCTCT 60
 TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTC GTTCTTACAA CCACCTGCAG 120
 GGTGACGTTC GTTGGCGTAA ACTGTTCTCT TTCACCAAAT ACTTCCTGAA AATCGAAAAA 180

AACGGTAAAG TTTCTGGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTCAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTTAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTTA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGACCTGCC AGGCTCTGGG TCAGGACATG GTTTCTCCGG AAGCTACCAA CTCTTCCTCT	60
TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTT GTTCTTACAA CCACCTGCAG	120
GGTGACGTTT GTTGGCGTAA ACTGTTCTCT TTCACCAAAT ACTTCCTGAA AATCGAAAAA	180
AACGGTAAAG TTTCTGGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTCAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTTAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTTA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGACCCTCAT GACCTCTCAG GCTCTGGGT

29

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGAGAACT CTCCGTACAG C

21

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTGTACGGT CTGTTCTCCT T

21

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC

35

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AAAGGATCCT GCCAGGCTCT GGGTCAGGAC ATG

33

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGGCCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCGGCGGTAC CTTATTATGA GTGTACCACC ATTGG

35

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA      60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG     120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC      180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTTAAC      240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT      300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG      360
AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC      420
TCATAA                                           426

```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1           5           10           15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20          25          30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35          40          45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50          55          60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65          70          75          80

```

Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
				85					90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
			100					105					110		
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys
		115					120					125			
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAACCACCTG CAGGGTGACG

20

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AACGGTCGAC AAATGTATGT GGCACCTGAAC GGTAAGGTG CTCCACGTCG TGGTCAGAAA

60

ACCCGTCGTA AAAACACC

78

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGCCCAAGC TTAAGAGTGT ACCACCATTG GCAGAAAGTG AGCAGAGGTG TTTTACGAC 60

GGGTTTTCTG ACCACG 76

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCACATACA TTTGTCGACC GTT 23

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGCCCAAGC TTAAGAGTG 19

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCCACATACA TTTGTCGACC GTT

23

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTGCAGGGTG ACGTTCGTTG GCGTAACTG TTCTCCTTCA CCAAATACTT CCTGAAAATC

60

GAAAAAAACG GTAAAGTTTC TGGTACCAAG

90

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGCTTTAACA GCAACAACAC CGATTTCAAC GGAGGTGATT TCCAGGATGG AGTACGGGCA

60

GTTTCTTTC TTGGTACCAG AAACCTTACC

90

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGTGTGTGTTG CTGTAAAGC TATCAACTCC AACTACTACC TGGCTATGAA CAAGAAAGGT 60
AAACTGTACG GTTCCAAAGA ATTTAACAAC 90

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCGACCGTT GTGCTGCCAG TTGAAGGAAG CGTAGGTGTT GTAACCGTTT TCTTCGATAC 60
GTTCTTTCAG TTTACAGTCG TTGTTAAATT CTTTGAACC 100

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCGGCGTCGA CCGTTGTGCT GCCAG 25

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCGGCCTGCA GGGTGACGTT CGTTGG

26

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CGCGCGATAT CTTATTAAGA GTGTACCACC ATTG

34

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC CTCACCAAA

60


```

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGTA CCAAGAAAGA AACTGCCCCG      120
TACTCCATCC TGGAAATCAC CTCCGTTGAA ATCGGTGTTG TTGCTGTAA AGCTATCAAC      180
TCCAACACTACT ACCTGGCTAT GAACAAGAAA GGTAACACTGT ACGGTTCCAA AGAATTTAAC      240
AACGACTGTA AACTGAAAGA ACGTATCGAA GAAAACGGTT ACAACACCTA CGCTTCCTTC      300
AACTGGCAGC ACAACGGTCG ACAAATGTAT GTGGCACTGA ACGGTAAAGG TGCTCCACGT      360
CGTGGTCAGA AAACCCGTCG TAAAAACACC TCTGCTCACT TTCTGCCAAT GGTGGTACAC      420
TCTTAA                                         426

```

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1              5              10              15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
          20              25              30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
          35              40              45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
          50              55              60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65              70              75              80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
          85              90              95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
          100              105              110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
          115              120              125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
          130              135              140

```

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGCGGCCCATG GCTCTGGGTC AGGACATG

28

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGGCCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGGCTCTGG GTCAAGATAT GGTTCCTCCG GAAGCTACCA ACTCTTCCTC TTCCTCTTTC	60
TCTTCCCCGT CTTCCGCTGG TCGTCACGTT CGTTCCTTACA ACCACCTGCA GGGTGACGTT	120
CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA	180

GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG TACAGCATCC TGGAGATAAC ATCAGTAGAA 240
 ATCGGAGTTG TTGCCGTCAA AGCCATTAAC AGCAACTATT ACTTAGCCAT GAACAAGAAG 300
 GGGAAACTCT ATGGCTCAAA AGAATTTAAC AATGACTGTA AGCTGAAGGA GAGGATAGAG 360
 GAAAATGGAT ACAATACCTA TGCATCATTT AACTGGCAGC ATAATGGGAG GCAAATGTAT 420
 GTGGCATTGA ATGGAAAAGG AGCTCCAAGG AGAGGACAGA AAACACGAAG GAAAAACACC 480
 TCTGCTCACT TTCTTCCAAT GGTGGTACAC TCATAA 516

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr	Asn	Ser	Ser	1	5	10	15
Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	Arg	His	Val	Arg	Ser	20	25	30	
Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	Ser	Phe	35	40	45	
Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	50	55	60	
Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	65	70	75	80
Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	85	90	95	
Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	100	105	110	
Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	115	120	125	
Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	130	135	140	
Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr				

145	150	155	160
Ser	Ala	His	Phe
Leu	Pro	Met	Val
Val	His	Ser	
165	170		

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTTTC 60
TCGTGTTTTTC TGTCC 75

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA      60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG     120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC      180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC      240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT      300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG      360
AGAGGACAGA AAACACGAGA AAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC      420
TCATAG                                     426

```

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1           5           10           15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20           25           30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35           40           45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50           55           60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65           70           75           80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85           90           95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100          105          110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Glu Lys
115          120          125

```

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCTG 60

TCGTGTTTTTC TGTCC 75

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGACA GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	1	5	10	15
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	20	25	30	
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	35	40	45	
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	50	55	60	
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	65	70	75	80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	85	90	95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	100	105	110	
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Gln	Lys	115	120	125	
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser	130	135	140				

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTCC TGTCCTCTCC TTGG 84

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGG AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	1	5	10	15
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	20	25	30	
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	35	40	45	
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	50	55	60	
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	65	70	75	80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	85	90	95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	100	105	110	
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Glu	Thr	Arg	Arg	Lys	115	120	125	
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser	130	135	140				

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTCTGC TGTCTCTCTCC TTGG 84

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

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AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC      240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT      300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG      360
AGAGGACAGC AGACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC      420
TCATAG                                          426

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(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1           5           10           15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20           25           30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35           40           45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50           55           60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65           70           75           80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85           90           95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100          105          110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Gln Thr Arg Arg Lys
115          120          125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130          135          140

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(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTTTC TGTCTTCCC TTGGAGCTCC TTT 93

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC 240

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AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT      300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG      360
GAAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC      420
TCATAG                                          426

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(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Met Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser
1           5           10           15

Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
20           25           30

Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val
35           40           45

Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu
50           55           60

Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn
65           70           75           80

Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
85           90           95

Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
100          105          110

Asn Gly Lys Gly Ala Pro Arg Glu Gly Gln Lys Thr Arg Arg Lys Asn
115          120          125

Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTTTC TGTCCCTGCC TTGGAGCTCC TTT 93

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAACTCT ATGGCTCAAA AGAATTTAAC 240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT 300

AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
 CAGGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
 TCATAG 426

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe			
1				5					10					15				
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser			
			20					25					30					
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser			
			35				40					45						
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr			
	50					55				60								
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn			
65				70					75						80			
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr			
			85					90					95					
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala			
			100					105					110					
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Gln	Gly	Gln	Lys	Thr	Arg	Arg	Lys			
		115					120					125						
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser						
	130					135					140							

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGAATGGAG AAGGAGCTCC A

21

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGGAGCTCCT TCTCCATTCA A

21

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGG

33

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTTAAC 240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT 300

AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAGAAGG AGCTCCAAGG 360

AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420

TCATAG 426

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	
		35					40					45				
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	
	50					55					60					
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	
	65				70					75					80	
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	
			85						90					95		
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	
			100					105					110			
Leu	Asn	Gly	Glu	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	
		115					120					125				
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser				
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540

TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCCTCTGCG TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGCGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTG ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCCTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCGTC	2220

TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCCGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTC	2700
GAACCCCAAG GTCCCCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760
GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGC GCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CCTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900

CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTACAC ATTAAGAGG 3960

AGAAATTACA TATG 3974

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC 60

CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG 112